STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	10/553, 406A
Source:	IFWO,
Date Processed by STIC:	11/08/2006
•	

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE <u>CHECKER</u> <u>VERSION 4.4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
 U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
 Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

	10/05 2061
ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 10/533, 906 A
	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s)contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
11Use of <220>	Sequence(s)missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown. Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13 Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

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DATE: 11/08/2006
                                            RAW SEQUENCE LISTING
                                                                                                                                     TIME: 13:21:22
                                            PATENT APPLICATION: US/10/553,906A
                                            Input Set: N:\Crf4\11082006\J533906A.raw On 10/21/05
Output Set: N:\CPR4\11082006\J533906A.raw
                                                                                                                                     Human Alkalinetabelow
                                            Output Set: N:\CRF4\11082006\J553906A.raw Was Omended to
                                                                                                                                        Spiningo mye lingse and
use of thereof the title
noes Not Comply
            1 <110> APPLICANT: Skanemejerier AB
            2 <120> TITLE OF INVENTION: NEW ENZYME AND ITS USE
            3 <130> FILE REFERENCE: 75086
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                                                                                                                                        Corrected Diskette Needed
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            5 <141> CURRENT FILING DATE: 2006-03-30
            6 <150> PRIOR APPLICATION NUMBER: US 60/320,139
            7 <151> PRIOR FILING DATE: 2003-04-24
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            9 <151> PRIOR FILING DATE: 2003-11-05
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                                                                                                         122137 Responses are Artificient the of the Service of Jenetic mater genetic grant great grant g
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           87
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 E--> 88
           89
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RAW SEQUENCE LISTING

DATE: 11/08/2006

PATENT APPLICATION: US/10/553,906A

TIME: 13:21:22

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	111 (
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E>		(900)
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	123	1140
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·	125 _ **	1200) Lactgggcat cgtgcccgag gccaacgatg ggcacctagc tactctgctg cccatgctgc 1260
臣>	126	1260
E>		and a grant contest toog cotgat got to too togget of ggacggacco tgcctcccca
	129	(1320)
E>	130	gettatecca ggccagagge tgcatgccac tgtccccggc agcgccaacc cctgcttggc
	131	1380
E>	132	tgttatggtg ctggtaataa gcctgcagcc caggtccaaa gcccccggcg agccggtccc
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/553,906A

DATE: 11/08/2006 TIME: 13:21:22

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Output Set: N:\CRF4\11082006\J553906A.raw

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	242	300			33		5555
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_	250	540					
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	252.	600					~~~~~~~~
E>	253 254	660	geeggaetee	acgggccaca	ggtacggccc	egagteeeeg	gagaggaggg
E>			acaaataaac	cggaccgtgg	gctacctccg	ggagaggatc	gcgcgcaacc
1 /	256	720	geaggeggae	cgguccgcgg	goodooog	334343444	303030000
E>			ccqcctcaac	ctgatcatca	catccgacca	cggcatgacg	accgtggaca
	258	780	.	J	J	<i>35 5 5</i>	5 55
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	264	960					
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E>			caaqqacatq	gacatgaaga	ccatcttccc	cactatagas	cctagettea
47	270	1140	caaggacacg	gacacgaaga	ccacccccg	0900909990	cooligottou
E>			ggaggtggag	ccctttgaga	gcgtccacgt	gtacgagete	atgtgccggc
	272	1200	33-33-33-3	3 - 3 -	3 - 3	5	5 5 55
E>	273	tgctgggcat	cgtgcccgag	gccaacgatg	ggcacctagc	tactctgctg	cccatgctgc
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	276	1320					
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	278	1380					1
E>			cgcataacgc	cccatggctc	aaggaagccg	ccgggagctg	cccgcaggcc /
_	280	1440	L _ L _ L				
E>			tgtctcgctg	cgatgctctg	ctggtcgcgg	acggaccctg	cccccagc /
	282	1500					

Same En

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/553,906A

DATE: 11/08/2006 TIME: 13:21:22

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Output Set: N:\CRF4\11082006\J553906A.raw

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/553,906A

VERIFICATION SUMMARYDATE: 11/08/2006PATENT APPLICATION: US/10/553,906ATIME: 13:21:23

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Output Set: N:\CRF4\11082006\J553906A.raw

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L:88 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:120 SEQ:2
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L:92 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:240 SEO:2
L:94 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:300 SEQ:2
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VERIFICATION SUMMARY

DATE: 11/08/2006 PATENT APPLICATION: US/10/553,906A TIME: 13:21:23

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L:291 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1800 SEQ:5
L:293 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1860 SEQ:5
L:295 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1878 SEQ:5
L:395 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:10
L:405 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:11
L:415 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:12
L:425 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:13
L:435 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:14
L:445 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:15
L:465 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:17
L:475 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEO:18
L:477 M:254 E: No. of Bases conflict, this line has no nucleotides.
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